

RAW SEQUENCE LISTING

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Application Serial Number: 10/713,578A
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RAW SEQUENCE LISTING

DATE: 02/16/2005

PATENT APPLICATION: US/10/713,578A

TIME: 16:20:22

Input Set : A:\124263-1006_US10.713578 SEQUENCE LISTING.ST25.txt

Output Set: N:\CRF4\02162005\J713578A.raw

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3 <110> APPLICANT: Awasthi, Sanjay
4   Singhal, Sharad S.
6 <120> TITLE OF INVENTION: Liposomes For Protection Against Toxic Compounds
8 <130> FILE REFERENCE: 124263-1006
10 <140> CURRENT APPLICATION NUMBER: US 10/713,578A
11 <141> CURRENT FILING DATE: 2003-11-13
13 <150> PRIOR APPLICATION NUMBER: 60/425,814
14 <151> PRIOR FILING DATE: 2002-11-13
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 655
22 <212> TYPE: PRT
23 <213> ORGANISM: artificial sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: recombinant protein expressed in E. coli
28 <400> SEQUENCE: 1
30 Met Thr Glu Cys Phe Leu Pro Pro Thr Ser Ser Pro Ser Glu His Arg
31 1           5           10           15
34 Arg Val Glu His Gly Ser Gly Leu Thr Arg Thr Pro Ser Ser Glu Glu
35           20           25           30
38 Ile Ser Pro Thr Lys Phe Pro Gly Leu Tyr Arg Thr Gly Glu Pro Ser
39           35           40           45
42 Pro Pro His Asp Ile Leu His Glu Pro Pro Asp Tyr Val Ser Asp Asp
43           50           55           60
46 Glu Lys Asp His Gly Lys Lys Lys Gly Lys Phe Lys Lys Lys Glu Lys
47 65           70           75           80
50 Arg Thr Glu Gly Tyr Ala Ala Phe Gln Glu Asp Ser Ser Gly Asp Glu
51           85           90           95
54 Ala Glu Ser Pro Ser Lys Met Lys Arg Ser Lys Gly Ile His Val Phe
55           100          105          110
58 Lys Lys Pro Ser Phe Ser Lys Lys Glu Lys Asp Phe Lys Ile Lys
59           115          120          125
62 Glu Lys Pro Lys Glu Glu Lys His Lys Glu Glu Lys His Lys Glu Glu
63           130          135          140
66 Lys His Lys Glu Lys Lys Ser Lys Asp Leu Thr Ala Ala Asp Val Val
67 145          150          155          160
70 Lys Gln Trp Lys Glu Lys Lys Lys Lys Lys Lys Pro Ile Gln Glu Pro
71           165          170          175
74 Glu Val Pro Gln Ile Asp Val Pro Asn Leu Lys Pro Ile Phe Gly Ile
75           180          185          190
78 Pro Leu Ala Asp Ala Val Glu Arg Thr Met Met Tyr Asp Gly Ile Arg
79           195          200          205

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82 Leu Pro Ala Val Phe Arg Glu Cys Ile Asp Tyr Val Glu Lys Tyr Gly
83      210      215      220
86 Met Lys Cys Glu Gly Ile Tyr Arg Val Ser Gly Ile Lys Ser Lys Val
87 225      230      235      240
90 Asp Glu Leu Lys Ala Ala Tyr Asp Arg Glu Glu Ser Thr Asn Leu Lys
91      245      250      255
94 Asp Tyr Glu Pro Asn Thr Val Ala Ser Leu Leu Lys Gln Tyr Leu Arg
95      260      265      270
98 Asp Leu Pro Glu Asn Leu Leu Thr Lys Glu Leu Met Pro Arg Phe Glu
99      275      280      285
102 Glu Ala Cys Gly Arg Thr Thr Glu Thr Glu Lys Val Gln Glu Phe Gln
103      290      295      300
106 Arg Leu Leu Lys Arg Leu Pro Glu Cys Asn Tyr Leu Leu Ile Ser Trp
107 305      310      315      320
110 Leu Ile Val His Met Asp His Val Ile Ala Lys Glu Leu Glu Thr Lys
111      325      330      335
114 Met Asn Ile Gln Asn Ile Ser Ile Val Leu Ser Pro Thr Val Gln Ile
115      340      345      350
118 Ser Asn Arg Val Leu Tyr Val Phe Phe Thr His Val Gln Glu Leu Phe
119      355      360      365
122 Gly Asn Val Val Leu Lys Gln Val Met Lys Pro Leu Arg Trp Ser Asn
123      370      375      380
126 Met Ala Thr Met Pro Thr Leu Pro Glu Thr Gln Ala Gly Ile Lys Glu
127 385      390      395      400
130 Glu Ile Arg Arg Gln Glu Phe Leu Leu Asn Cys Leu His Arg Asp Leu
131      405      410      415
134 Gln Gly Gly Ile Lys Asp Leu Ser Lys Glu Lys Arg Leu Trp Glu Val
135      420      425      430
138 Gln Arg Ile Leu Thr Ala Leu Lys Arg Lys Leu Arg Glu Ala Lys Arg
139      435      440      445
142 Gln Glu Cys Glu Thr Lys Ile Ala Gln Glu Ile Ala Ser Leu Ser Lys
143      450      455      460
146 Glu Asp Val Ser Lys Glu Glu Met Asn Glu Asn Lys Glu Val Ile Asn
147 465      470      475      480
150 Ile Leu Leu Ala Gln Glu Asn Glu Ile Leu Thr Glu Gln Glu Glu Leu
151      485      490      495
154 Leu Ala Asn Glu Gln Phe Leu Arg Arg Gln Ile Ala Ser Glu Lys Glu
155      500      505      510
158 Glu Ile Glu Arg Leu Arg Ala Glu Ile Ala Glu Ile Gln Ser Arg Gln
159      515      520      525
162 Gln His Gly Arg Ser Glu Thr Glu Glu Tyr Ser Ser Glu Ser Glu Ser
163      530      535      540
166 Glu Ser Glu Asp Glu Glu Glu Leu Gln Ile Ile Leu Glu Asp Leu Gln
167 545      550      555      560
170 Arg Gln Asn Glu Glu Leu Glu Ile Lys Asn Asn His Leu Asn Gln Ala
171      565      570      575
174 Ile His Glu Glu Arg Glu Ala Ile Ile Glu Leu Arg Val Gln Leu Arg
175      580      585      590
178 Leu Leu Gln Met Gln Arg Ala Lys Ala Glu Gln Gln Ala Gln Glu Asp

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179          595          600          605
182 Glu Glu Pro Glu Trp Arg Gly Gly Ala Val Gln Pro Pro Arg Asp Gly
183          610          615          620
186 Val Leu Glu Pro Lys Ala Ala Lys Glu Gln Pro Lys Ala Gly Lys Glu
187 625          630          635          640
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195 <211> LENGTH: 1974
196 <212> TYPE: DNA
197 <213> ORGANISM: artificial sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: human bone marrow cDNA library
202 <400> SEQUENCE: 2
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207 ttgtaccgca ctggcgagcc ctcacctccc catgacatcc tcatgagcct cctgatgtag      180
209 tgtctgatga tgagaaagat catgggaaga aaaaaggga atttaagaaa aaggaaaaga      240
211 ggactgaagg ctatgcagcc tttcaggaag atagctcttg agatgaggca gaaagtcctt      300
213 ctaaaatgaa gaggtccaag ggaatccatg ttttcaagaa gaagcccagc ttttctaaaa      360
215 agaaggaaaa ggatttttaa ataaaagaga aacccaaaga agaaaagcat aaagaagaaa      420
217 gcacaaagaa gaaaaacata aagagaagaa gtcaaaagac ttgacagcag ctgatgttgt      480
219 taaacagtgg aaggaaaaga agaaaaagaa aaagccaatt caggagccag aggtgcctca      540
221 gattgatgtt ccaaattctc aaccattttt tgggaattcct ttggctgatg cagtagagag      600
223 gaccatgatg tatgatggca ttcggtgcc agcgtttt cgtgaatgta tagattacgt      660
225 agagaagtat ggcataagat gtgaaggcat ctacagagta tcaggaatta aatcaaaggt      720
227 ggatgagcta aaagcagcct atgaccggga ggagtctaca aacttggaag actatgagcc      780
229 taacactgta gccagtttgc tgaagcagta ttgcgagac cttccagaga atttgcttac      840
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233 gcaggaattc cagcgtttac tcaaagaact gccagaatgt aactatcttc tgatttcttg      960
235 gctcattgtg cacatggacc atgtcattgc aaaggaactg gaaacaaaaa tgaatataca     1020
237 gaacatttct atagtgtctc gcccaactgt gcagatcagc aatcgagtcc tgtatgtgtt     1080
239 tttcacacat gtgcaagaac tctttggaaa tgtggtacta aagcaagtga tgaaacctct     1140
241 gcgatggtct aacatggcca cgatgccac gctgccagag acccaggcgg gcatcaagga     1200
243 ggagatcagg agacaggagt ttcttttgaa ttgtttacat cgagatctgc aggggtgggat     1260
245 aaaggatttg tctaaagaag aaagattatg ggaagtacaa agaattttga cagccctcaa     1320
247 aagaaaactg agagaagcta aaagacagga gtgtgaaacc aagattgcac aagagatagc     1380
249 cagtctttca aaagaggatg tttccaaaga agagatgaat gaaaatgaag aagttataaa     1440
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255 gattgctgaa attcagagtc gccagcagca cggccgaagt gagactgagg agtactcttc     1620
257 cgagagcgag agcgagagtg aggatgagga ggagctgcag atcattctgg aagacttaca     1680
259 gagacagaac gaagagctgg aaataaagaa caatcatttg aatcaagcaa ttcatagagga     1740
261 gcgcgaggcc atcatcgagc tgcgcgtgca gctgcggctg ctccagatgc agcgagccaa     1800
263 ggccgagcag caggcgagcagg aggacgagga gcctgagtgg cgcgggggtg ccgtccagcc     1860
265 gccagagac ggcgtccttg agccaaaagc agctaaagag cagccaaagg caggcaagga     1920
267 gccggcaaag ccatcgccca gcagggatag gaaggagacg tccatctgad aasv      1974

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